SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Use of genes for increasing the oil content in plants

<130> PF54384

<140> AE20020908
<141> 2003-04-14

<160> 35

<170> PatentIn Ver. 2.1

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<212> DNA
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tat ccc aga aga agc ccc ctt tgg aga ttt ctt tca tac agt aca tca   96
Tyr Pro Arg Arg Ser Pro Leu Trp Arg Phe Leu Ser Tyr Ser Thr Ser
            20                  25                  30

tta ctg acc ttc ggt gta tca aaa ctg ctt ctt ttc aca tgc tat aat   144
Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
        35                  40                  45

gtc aaa ttg aat ggt ttt gaa aaa tta gaa act gcc ttg gaa cgt tcc   192
Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
    50                  55                  60

aaa agg gaa aat aga ggc ctt atg acg gtc atg aac cat atg agt atg   240
Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
65                  70                  75                  80

gtc gat gat ccg tta gtt tgg gca aca cta cca tat aag tta ttt acg   288
Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
                85                  90                  95

tct ttg gac aac ata aga tgg tct ttg ggt gca cat aat att tgc ttt   336
Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
            100                 105                 110

caa aat aaa ttt ctg gcc aac ttt ttc tca ctt ggc caa gtc ctt tca   384
Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
        115                 120                 125

aca gaa aga ttt ggg gtg ggc cca ttt caa ggt tct ata gat gct tca   432
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ata aga ttg tta agc cct gac gac act tta gac ttg gaa tgg acc cct   480
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145                 150                 155                 160

cac tct gag gtc tct tct tcg cta aaa aaa gcc tac tcc ccg ccc ata   528
His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
                165                 170                 175

ata agg tcg aag cca tct tgg gtc cat gtt tat cca gaa gga ttt gta   576
Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
            180                 185                 190

cta caa tta tat ccg cct ttt gaa aat tcg atg agg tat ttt aaa tgg   624
Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
        195                 200                 205

ggt att acc aga atg atc cta gaa gca aca aag ccg ccc att gta gta   672
Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
    210                 215                 220

cca ata ttt gct aca ggg ttt gaa aaa ata gca tcc gaa gca gtc aca   720
Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
225                 230                 235                 240

gat tca atg ttt aga caa att cta cca aga aac ttt ggc tct gaa ata   768
Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
                245                 250                 255

aat gtt acc ata ggg gat cct tta aat gat gat tta atc gac agg tat   816
Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
            260                 265                 270

aga aaa gaa tgg aca cat ttg gtt gaa aaa tac tat gat ccc aaa aat   864
Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
        275                 280                 285

cct aac gac ctc tct gac gaa ttg aaa tat ggt aaa gag gcg caa gat   912
Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
    290                 295                 300

tta aga agc aga tta gcc gct gaa ctg aga gcc cat gtt gct gaa att   960
Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
305                 310                 315                 320

aga aat gaa gtt cgc aaa tta cca cgc gaa gac cct agg ttc aaa tcc  1008
Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
                325                 330                 335

ccc tca tgg tgg aag cgg ttc aac acc acg gaa ggt aaa tcg gac cca  1056
Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
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gat gtt aaa gtc att ggc gaa aat tgg gca ata agg agg atg caa aag  1104
Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
        355                 360                 365
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Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
50 55 60
Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
65 70 75 80
Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
85 90 95
Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
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Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
115 120 125
Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
130 135 140
Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
145 150 155 160
His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
165 170 175
Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
180 185 190
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195 200 205

Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
210 215 220
Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
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Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
245 250 255
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260 265 270
Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
275 280 285
Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
290 295 300
Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
305 310 315 320
Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
325 330 335
Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
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370 375 380

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ctg ttg ttc aat ctt aaa ctt cgt gat cga ttt cga atc gcc gtc gat   97
Leu Leu Phe Asn Leu Lys Leu Arg Asp Arg Phe Arg Ile Ala Val Asp
                   20                  25                  30

gat cac cgt ggt cga gct acg gtt ttc tca ccg gat ggt tgc ttc tct  145
Asp His Arg Gly Arg Ala Thr Val Phe Ser Pro Asp Gly Cys Phe Ser
               35                  40                  45

tcc act atc cac cgc tgg gtg act cga ttc cgg aac ttt cgc cgg gag  193
Ser Thr Ile His Arg Trp Val Thr Arg Phe Arg Asn Phe Arg Arg Glu
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tct ctc cct tct cca ccg gct ttt tat cgc aga cga gtt tct aag gac  241
Ser Leu Pro Ser Pro Pro Ala Phe Tyr Arg Arg Arg Val Ser Lys Asp
       65                  70                  75

tta acg gca gaa gaa gag tct gct ctt ttc cgg atg cta caa act gtg  289
Leu Thr Ala Glu Glu Glu Ser Ala Leu Phe Arg Met Leu Gln Thr Val
   80                  85                  90                  95

gct gtt ccc ctt att gga aat gct tgt cat gtt ttc atg aat ggt ttt  337
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aac cgt gtt cag gta tat ggt tta gag aaa ttg cat gat gct tta ctc  385
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           115                 120                 125

aac aga cca aag aac aag cct ctt gta acg gtg agc aat cat gtt gca  433
Asn Arg Pro Lys Asn Lys Pro Leu Val Thr Val Ser Asn His Val Ala
       130                 135                 140

tct gtg gat gat cca ttt gtc att gct tca tta ctt cca cct aaa ttt  481
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cta ctt gat gcc cgt aat ttg agg tgg acg ctc tgt gct aca gat aga  529
Leu Leu Asp Ala Arg Asn Leu Arg Trp Thr Leu Cys Ala Thr Asp Arg
160                 165                 170                 175

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gcg att tcg aaa ttg aac aac gga ggg tgg gtt cac atc ttt cca gaa   673
Ala Ile Ser Lys Leu Asn Asn Gly Gly Trp Val His Ile Phe Pro Glu
        210                 215                 220

ggc agt cgc tcc cgg gat ggt gga aag act atg ggc tca gcg aag agg   721
Gly Ser Arg Ser Arg Asp Gly Gly Lys Thr Met Gly Ser Ala Lys Arg
    225                 230                 235

ggt atc gga agg ttg att ttg gac gca gat act ctc cct atg gtt gtt   769
Gly Ile Gly Arg Leu Ile Leu Asp Ala Asp Thr Leu Pro Met Val Val
240                 245                 250                 255

cct ttt gtg cat act ggt atg cag gat ata atg cca gtt gga gct agt   817
Pro Phe Val His Thr Gly Met Gln Asp Ile Met Pro Val Gly Ala Ser
                260                 265                 270

gtt cca cgg att ggc aag aca gtg aca gtg atc att gga gac cct att   865
Val Pro Arg Ile Gly Lys Thr Val Thr Val Ile Ile Gly Asp Pro Ile
            275                 280                 285

cat ttt aat gac att ctc agc act gaa gga gcc caa cac gtc tca agg   913
His Phe Asn Asp Ile Leu Ser Thr Glu Gly Ala Gln His Val Ser Arg
        290                 295                 300

aaa cac ctg tat gac gcc gtt tcg tcc aga att gga caa aga ctg tac   961
Lys His Leu Tyr Asp Ala Val Ser Ser Arg Ile Gly Gln Arg Leu Tyr
    305                 310                 315

gat tta aaa gca caa gtt gat aga gta tat ata gaa caa caa tct atg   1009
Asp Leu Lys Ala Gln Val Asp Arg Val Tyr Ile Glu Gln Gln Ser Met
320                 325                 330                 335

atg tca cac aat gcc aaa aca ccc tcg gac cgt gct gct gag atc ttt   1057
Met Ser His Asn Ala Lys Thr Pro Ser Asp Arg Ala Ala Glu Ile Phe
                340                 345                 350

cat aga gtc gat tgg gac tca ttt ggg atg gga gca caa ttt tca gaa   1105
His Arg Val Asp Trp Asp Ser Phe Gly Met Gly Ala Gln Phe Ser Glu
            355                 360                 365

gaa tca tca ccc agt agt aaa ccg att ggc caa agc gat gat cgc att   1153
Glu Ser Ser Pro Ser Ser Lys Pro Ile Gly Gln Ser Asp Asp Arg Ile
        370                 375                 380

gtc aga tct ccc aaa agg aga gtc tca ccc gaa gga ggg gtc agc ttg   1201
Val Arg Ser Pro Lys Arg Arg Val Ser Pro Glu Gly Gly Val Ser Leu
    385                 390                 395

aag att aag aag ctc atg gac tca acc gag atg atg ggg ttt gcg gct   1249
Lys Ile Lys Lys Leu Met Asp Ser Thr Glu Met Met Gly Phe Ala Ala
400                 405                 410                 415
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aga ggg tta cta atg aac gag tac aag agt cgg gtt gaa tct gcc aat 1297
Arg Gly Leu Leu Met Asn Glu Tyr Lys Ser Arg Val Glu Ser Ala Asn
420 425 430

gtt ggt agg cct tta aag gct tgg aga gag tat ttt atg aac cgt gga 1345
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35 40 45

Thr Ile His Arg Trp Val Thr Arg Phe Arg Asn Phe Arg Arg Glu Ser
50 55 60

Leu Pro Ser Pro Pro Ala Phe Tyr Arg Arg Arg Val Ser Lys Asp Leu
65 70 75 80

Thr Ala Glu Glu Glu Ser Ala Leu Phe Arg Met Leu Gln Thr Val Ala
85 90 95

Val Pro Leu Ile Gly Asn Ala Cys His Val Phe Met Asn Gly Phe Asn
100 105 110

Arg Val Gln Val Tyr Gly Leu Glu Lys Leu His Asp Ala Leu Leu Asn
115 120 125

Arg Pro Lys Asn Lys Pro Leu Val Thr Val Ser Asn His Val Ala Ser
130 135 140

Val Asp Asp Pro Phe Val Ile Ala Ser Leu Leu Pro Pro Lys Phe Leu
145 150 155 160

Leu Asp Ala Arg Asn Leu Arg Trp Thr Leu Cys Ala Thr Asp Arg Cys
165 170 175

Phe Lys Asn Pro Val Thr Ser Ala Phe Ser Arg Ser Val Lys Val Leu
180 185 190

Pro Ile Ser Arg Gly Glu Gly Ile Tyr Gln Gln Gly Met Asp Ile Ala
195 200 205

Ile Ser Lys Leu Asn Asn Gly Gly Trp Val His Ile Phe Pro Glu Gly
210 215 220

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Ser Arg Ser Arg Asp Gly Gly Lys Thr Met Gly Ser Ala Lys Arg Gly
225                 230                 235                 240

Ile Gly Arg Leu Ile Leu Asp Ala Asp Thr Leu Pro Met Val Val Pro
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Phe Val His Thr Gly Met Gln Asp Ile Met Pro Val Gly Ala Ser Val
            260                 265                 270

Pro Arg Ile Gly Lys Thr Val Thr Val Ile Ile Gly Asp Pro Ile His
        275                 280                 285

Phe Asn Asp Ile Leu Ser Thr Glu Gly Ala Gln His Val Ser Arg Lys
    290                 295                 300

His Leu Tyr Asp Ala Val Ser Ser Arg Ile Gly Gln Arg Leu Tyr Asp
305                 310                 315                 320

Leu Lys Ala Gln Val Asp Arg Val Tyr Ile Glu Gln Gln Ser Met Met
                325                 330                 335

Ser His Asn Ala Lys Thr Pro Ser Asp Arg Ala Ala Glu Ile Phe His
            340                 345                 350

Arg Val Asp Trp Asp Ser Phe Gly Met Gly Ala Gln Phe Ser Glu Glu
        355                 360                 365

Ser Ser Pro Ser Ser Lys Pro Ile Gly Gln Ser Asp Asp Arg Ile Val
    370                 375                 380

Arg Ser Pro Lys Arg Arg Val Ser Pro Glu Gly Gly Val Ser Leu Lys
385                 390                 395                 400

Ile Lys Lys Leu Met Asp Ser Thr Glu Met Met Gly Phe Ala Ala Arg
                405                 410                 415

Gly Leu Leu Met Asn Glu Tyr Lys Ser Arg Val Glu Ser Ala Asn Val
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Trp Ala Ala Arg Ser Asp His Leu Gly Gly Ile Pro Arg Asn Thr Val
            10                  15                  20

ata atg gct gtt agt gca ttt gca aaa gca gta gca aat ctt tgc aat   151
Ile Met Ala Val Ser Ala Phe Ala Lys Ala Val Ala Asn Leu Cys Asn
        25                  30                  35

aaa agc tca gtt cac aat gca gat act ctt atg aat ctt gtc cag tca   199
Lys Ser Ser Val His Asn Ala Asp Thr Leu Met Asn Leu Val Gln Ser
    40                  45                  50

aga cca cct ggt gtt cct ctc atc act gtt agt aat cac atg tcg act   247
Arg Pro Pro Gly Val Pro Leu Ile Thr Val Ser Asn His Met Ser Thr
55                  60                  65                  70

ttg gat gat cca gta atg tgg ggg gca ttt aag ggt ctc ctt tcc tta   295
Leu Asp Asp Pro Val Met Trp Gly Ala Phe Lys Gly Leu Leu Ser Leu
                75                  80                  85

gat cca gaa ttg gct cgg tgg gtt ctt gct gca gag gat ata tgt ttc   343
Asp Pro Glu Leu Ala Arg Trp Val Leu Ala Ala Glu Asp Ile Cys Phe
            90                  95                  100

agg aac cct ata ttc tcc tac att ttc cgc act gga aaa tgt ata cct   391
Arg Asn Pro Ile Phe Ser Tyr Ile Phe Arg Thr Gly Lys Cys Ile Pro
        105                 110                 115

ata act aga ggt ggt gga atc tac caa gaa aac atg aat gaa gct ctc   439
Ile Thr Arg Gly Gly Gly Ile Tyr Gln Glu Asn Met Asn Glu Ala Leu
    120                 125                 130

cag cga tta aaa gat gga tct tgg ctg cat acc ttc cca gag gga aag   487
Gln Arg Leu Lys Asp Gly Ser Trp Leu His Thr Phe Pro Glu Gly Lys
135                 140                 145                 150

gtg ttt caa gat gat gtt cct ata aga cga ctt aaa tgg gga act gca   535
Val Phe Gln Asp Asp Val Pro Ile Arg Arg Leu Lys Trp Gly Thr Ala
                155                 160                 165

agc ctc atc gcc cgt tcc cca gtt acc cca atc gtt ttg cca ata att   583
Ser Leu Ile Ala Arg Ser Pro Val Thr Pro Ile Val Leu Pro Ile Ile
            170                 175                 180

cac cgt ggt ttt gag gag atg atg ccg gag aac tac aat aat gga cga   631
His Arg Gly Phe Glu Glu Met Met Pro Glu Asn Tyr Asn Asn Gly Arg
        185                 190                 195

aga cca ctg gta ccg ttg ccg aac aaa cac ctt aaa gtt gtg gtt ggt   679
Arg Pro Leu Val Pro Leu Pro Asn Lys His Leu Lys Val Val Val Gly
    200                 205                 210

gaa cca att gag ttt gat gtt cca atg atg gtt gag act gct gtc ttg   727
Glu Pro Ile Glu Phe Asp Val Pro Met Met Val Glu Thr Ala Val Leu
215                 220                 225                 230

gac tcc cgc cat gta acc cct cct ctt caa gaa gtg aaa tgg cct gtc   775
Asp Ser Arg His Val Thr Pro Pro Leu Gln Glu Val Lys Trp Pro Val
                235                 240                 245
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ctc act tct gct ggc caa gtg cta gac gaa act gct cag aga cac ctc   823
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            250                 255                 260

tac ata gct ctg tcc gag aag att caa tcc tcc ttg gaa aca ttg aga   871
Tyr Ile Ala Leu Ser Glu Lys Ile Gln Ser Ser Leu Glu Thr Leu Arg
        265                 270                 275

ctc tta gcc aag cgg ttg tgacttccgc cgggaaactt catatcaaaa           919
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Val Ala Asn Leu Cys Asn Lys Ser Ser Val His Asn Ala Asp Thr Leu
        35                  40                  45

Met Asn Leu Val Gln Ser Arg Pro Pro Gly Val Pro Leu Ile Thr Val
    50                  55                  60

Ser Asn His Met Ser Thr Leu Asp Asp Pro Val Met Trp Gly Ala Phe
65                  70                  75                  80

Lys Gly Leu Leu Ser Leu Asp Pro Glu Leu Ala Arg Trp Val Leu Ala
                85                  90                  95

Ala Glu Asp Ile Cys Phe Arg Asn Pro Ile Phe Ser Tyr Ile Phe Arg
            100                 105                 110

Thr Gly Lys Cys Ile Pro Ile Thr Arg Gly Gly Gly Ile Tyr Gln Glu
        115                 120                 125

Asn Met Asn Glu Ala Leu Gln Arg Leu Lys Asp Gly Ser Trp Leu His
    130                 135                 140

Thr Phe Pro Glu Gly Lys Val Phe Gln Asp Asp Val Pro Ile Arg Arg
145                 150                 155                 160

Leu Lys Trp Gly Thr Ala Ser Leu Ile Ala Arg Ser Pro Val Thr Pro
                165                 170                 175

Ile Val Leu Pro Ile Ile His Arg Gly Phe Glu Glu Met Met Pro Glu
            180                 185                 190

Asn Tyr Asn Asn Gly Arg Arg Pro Leu Val Pro Leu Pro Asn Lys His
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195 200 205

Leu Lys Val Val Val Gly Glu Pro Ile Glu Phe Asp Val Pro Met Met
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225 230 235 240

Glu Val Lys Trp Pro Val Leu Thr Ser Ala Gly Gln Val Leu Asp Glu
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ctccgcgttg ctgcatagac ctaagggcaa acctcttctt acggtcagca atcatgttgc 360
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tan 423

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aaagaggtgt tggaaggttg gtacttgatg ctgatacttc tccccattgt agtcccggtc 360
gtgcacac 368

<210> 11
<211> 376
<212> DNA
<213> Linum usitatissimum

<220>
<221> misc_feature
<222> (1)..(376)

<400> 11
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tcttacttct ttcgcatggg gaaatgtatt cccattacaa gaggtggggg aatttatcgg 360
agccacatga atgaag 376

<210> 12
<211> 418
<212> DNA
<213> Linum usitatissimum

<220>
<221> misc_feature
<222> (1)..(418)

<400> 12
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atgtggggat tcaagggatt cccaatcatg aatgcgaaat tgtttcgatg ggtattagct 120
gctgaagaca tctgtttcag gaattctttt cattcttact tctttcgcat ggggaaatgt 180
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cctataagac gattgaaatg gggaactgcc agtctcatcg tccgtgcccc tgttacaccg 360
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<210> 13
<211> 445
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(445)

<400> 13
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gactcgttgc cgtcgtccac ctcttttttat cgcaaacgag tgattaagga tttcagttct 180
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cactccgctt tactgcaaag acctaaagga aaacctcttc ttacggtcag caatcatgtt 360
gcttccatgg atgatcctct tgttattgct tcgctgcttc ctccgagtgt tcttttggac 420
gctaggaatc tcagatggac gcttc 445

<210> 14
<211> 361
<212> DNA
<213> Hordeum vulgare

<220>
<221> misc_feature
<222> (1)..(361)

<400> 14
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ggcattgctt gagaggccta aggacaagcc cctagtaacg gttagcaacc atgttgcttc 180
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gaacttgagg tggacacttt gcgcaacgat cgctgtttta ggaatcccgt cacttctgca 300
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<210> 15
<211> 472
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(472)

<400> 15
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gttacttctc ttcctccatc caccgcttgg ctgctcgatt gcggaacttc cgccgcgagt 120
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gtcatgtttt catgaatggt cttaaccgtg ttcaggtgta tggtttagag aagttgcatg 300
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ccttggatga tccatttgtc attgcttcgt tacttccgcc taagcttcta ctcgatgctc 420
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<210> 16
<211> 412
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(412)

<400> 16
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tcttccgcac tggcaagtgt atacctataa ctagaggtgg tggaatctac caagaacaca 180
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cccgttgccc agtcacccca atcgtcttgc caataattca ccgtggtttg acgagatgaa 360
tgccgagagt acatttatgg aaaangacca ccgtacccgt tgggaacaaa an 412

<210> 17
<211> 410
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(410)

<400> 17
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ggctcgatgg gttcttgctg cagaggacat ttgtttcaag aaccctgtct tctcctacat 120
cttccgcact ggcaagtgta tacctataac tagaggtggt ggaatctacc aagaacacat 180
gagtgaagct ctcgagcgat taaaagatgg atcttggttg cataccttcc cagagggcaa 240
ggtgtttcaa gaagatgtgc ctataagacg acttaaatgg ggaaccgcaa gcctcatcgc 300
ccgttgccca gtcacccaaa tcgtcttgcc aatatttcac cgtggttttg acaacatgat 360
gcccgaaaat gtccttttat ggaagaatga caaccgtacc tgtggggaan 410

<210> 18

<211> 420
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(420)

<400> 18
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cgtccacctc tttttatcgc atacgagtga ttaaggattt cagttctgaa gaagattcaa 180
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tgcaaagacc taaaggaaaa cctcttctta cggtcagcaa tcatgttgct tccatggatg 360
atcctcttgt tattgcttcg ctgcttcctc cgagtgttct tttggacgct aggaatctcn 420

<210> 19
<211> 490
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(490)

<400> 19
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aggtattgga aggttgattt tggacgcaga taccctccct atggttgttc catttgtgca 120
tactggtatg caagatataa tgcctatagg agccagtgtt ccacggattg gcaaaacagt 180
gacagtgatc attggagatc ctattccctt taatgacctt gtagacactg aaggagccaa 240
acacgtttca aggaagcagt tgtatgacgc tgtatcttcc aggataggac aaagattaca 300
ccagttaaag caacaggttg ataaagtatc tctgggagca caatattcag aagaatcacc 360
agcccttctt ggtaaacaaa tttcccaaac cgatgtncgt ctcaatggtt tggactggca 420
tgttcctaaa agggattgcc atccgaagga agcatcagcc tgaaggttaa gaggtttatg 480
gactctacag 490

<210> 20
<211> 386
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (1)..(386)

<400> 20
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tcagccgatt agaagattga agtggggaac ggccagtctt attgtccgag cacctataac 120
tccaatagtt ttgccaattg ttcactctgg tttcgaaaag gtcatgccag aaaactcgtt 180
ctttggacgg cgaccaccgg tgccactctg cagtaagaag atagacatca ttgttggaga 240
gccaatagag tttgacttgc caagcttgaa gcaagaagca tcaacggtac cccatgactc 300
atcctctgaa cggaaggggt ggccggccat tacaccagat gggctggacg aggccgccca 360
gagatggctt taccagaaga tgtcag 386

<210> 21

<211> 429
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(429)

<400> 21
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tatgatgctc tgctcaacag gccaaagaac aagcctctcg taacggctaa caatgatgtg 120
gcatccttgg atgatccatt cgccattgct tcattactat ccgcctaagc ttctactctg 180
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cagaaggcag acggtaccga gatggtggct agactatggg ttcacgcaat agaggtattg 420
gaatgttgt 429

<210> 22
<211> 436
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(436)

<400> 22
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tttccgcact gacacgcgta tacctataac tagaggtggt ggaatctacc aagaacacat 180
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ccaatcgtct tgccaataat tcaccgtggt tctgacgaga tgatgccgga gaagtacatt 360
tatggaagaa taccaccgtt accgctgtgg aacaaaaacc ttaaagtagt tgttggtgaa 420
ccaatcagag ttgatg 436

<210> 23
<211> 423
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(423)

<400> 23
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tttgaggtgg acgctttgtg ctacagatag atgcttcaaa aaccctgtaa cttcagcttt 120
ctttcgatcc gtcaaggttt tgccagtttc tcgcggtgaa ggaatttatc agcagggaat 180
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tttggacgca gataccctcc ctaatgttgt tccatttgtg catactggta tgcaagatat 360
aatgcctata ggagccagtg ttccacggat tggcaaaaca gtgacagtga tcattggaga 420
tcn 423

<210> 24
<211> 400
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(400)

<400> 24
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gcgatgaaac ccaacacatc tctagaggca ttttgtatga caaagcaaca gaaaggattg 360
ggcagagact gcaggaactg aaagccgaag tcgatagatt 400

<210> 25
<211> 414
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(414)

<400> 25
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tcttatgact cttgtccgtt cacgaccacc tggtgtccct ctcatcactt ttagatgatc 180
cagtaatgtg gggagggttc aagggtcttc tttctttaga tccagagttg gctcgatggg 240
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gcaagtgtat acctataact agaggtggtg gaatctatca agaacacatg agtgaagctc 360
ttgaacgatt aaaagatgga tcttggttgc ataccttccc agaggggcag gtgg 414

<210> 26
<211> 397
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(397)

<400> 26
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ctatcttccg gatgcttcaa gctgtggctg ttccacttat tggaaacgct tgtcatgttt 120
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ggtggacgct ttgtgctaca gatagatgct ttaagaaccc tgtaacttca gctttctttc 360
gatccgtcaa agttttgcca gtttctcgcg gtgaagg 397

<210> 27
<211> 429

<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(429)

<400> 27
gaattcaacg tcgacgattt cgtcgatccg tcaaggtttt gccagtttct cgcggtgaag 60
gaatttatca gcagggaatg gacattgcga tttcgaaatt gaataatgga ggatgggttc 120
acatatttcc agaaggtagt cgctcccgag atggtggcaa gactatgggc tcagcaaaaa 180
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tgacagtgat cattggagat cctattccct ttagtgacct tgtagacact gaacgatcca 360
aacacgtttc aaggaaccag gtttatgacc ctctatcgtt caggatcgac agcgattacc 420
ctcctgcat 429

<210> 28
<211> 404
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(404)

<400> 28
gttacttccg cctaagcttc tactcgatgc tcgtaatttg aggtggacgc tttgtgctac 60
agatagatgc ttcaaaaacc ctgtaacttc agctttcttt cgatccgtca aggttttgcc 120
agtttctcgc ggtgaaggaa tttatcagca gggaatggac attgcgattt cgaaattgaa 180
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<210> 29
<211> 467
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(467)

<400> 29
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tttcacggcg actgtgacga catcatgacg cagaaggcca tggatctata aacaccaccg 420
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<210> 30
<211> 459

<212> DNA
<213> Brassica napus

<220>
<221> misc_difference
<222> (1)..(459)

<400> 30
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tgggctacac acagatggtt taccaaccct gtgcttccg 459

<210> 31
<211> 389
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(389)

<400> 31
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ctttatcccc tctgccgatg gctacttctc ctcgaccatt caacgctgcc tcagccgatt 120
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tggtttagaa aaactgcact ccgcgttgct gcatagacct aagggcaaac ctcttcttac 360
ggtcagcaat catgttgctt ccatggatg 389

<210> 32
<211> 400
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(400)

<400> 32
agaaaaactg cactccgctt tactgcaaag acctaaagga aaacctcttc ttacggtcag 60
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gatattccca cacggcggtt gatccctcta tttttcaaaa tcagaaagtt aaaataaggg 360
agggggcgtc gaaaaatcca agcggggagc gggccccttg 400

<210> 33
<211> 449
<212> DNA

<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(449)

<400> 33
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aggtggacgc tntgtgctac agatagatg 449

<210> 34
<211> 429
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(429)

<400> 34
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tgtaggtgct aactttccca gaataggcaa gatggttaca gtgctcatag gtgatccgat 180
caattttgat gatataattg aatttgacaa agacanaggc tcaaatgtgc ccagaagacg 240
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tgacactatc gcaattgtca agaaatgcag gtaccagaaa agtcctcaca cagactgacc 360
gaccattaaa aaactgagcc aggtgattgg gactaatttg aatggacatc ttctggccgc 420
agaaatgcc 429

<210> 35
<211> 449
<212> DNA
<213> Brassica napus

<220>
<221> misc_feature
<222> (1)..(449)

<400> 35
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tcctcctcca tccaccgctt ggctgctcga ttccggaact tccgccgcga gtctctccct 120
tctgcccccg ctttttatcg cagaagagta cctaaagatt tgacggcaga agaagagtct 180
gctatcttcc ggatgcttca agctgtggct gttccactta ttggaaacgc ttgtcatgtt 240
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